1642

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         RAW SEQUENCE LISTING                   DATE: 06/18/2002
         PATENT APPLICATION:   US/09/558,741    TIME: 07:58:57

         Input Set : N:\Crf3\Datahold\EFS\09558741\CIBT-P01-130SequenceListing.txt
         Output Set: N:\CRF3\06182002\I558741.raw

    5 <110> APPLICANT: Huston, J.
    6        Houston, L.L.
    7        Ring, D.
    8        Oppermann, H.
   10 <120> TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
   12 <130> FILE REFERENCE: CIBT-P01-130
   14 <140> CURRENT APPLICATION NUMBER: 09/558,741
   15 <141> CURRENT FILING DATE: 2000-04-26
   17 <150> PRIOR APPLICATION NUMBER: 07/831,967
   18 <151> PRIOR FILING DATE: 1992-02-06
   20 <160> NUMBER OF SEQ ID NOS: 16
   22 <170> SOFTWARE: PatentIn version 3.1
   24 <210> SEQ ID NO: 1
   25 <211> LENGTH: 909
   26 <212> TYPE: DNA
   27 <213> ORGANISM: Artificial Sequence
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   30 <223> OTHER INFORMATION: 741F8 sFv'
   32 <220> FEATURE:
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   34 <222> LOCATION: (3)..(752)
   35 <223> OTHER INFORMATION:
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   40    1               5                  10                  15
   42 cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc        95
   43 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
   44               20                  25                  30
   46 aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta       143
   47 Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
   48               35                  40                  45
   50 aag tgg atg ggc tgg ata aac acc aac act gga gag cca aca tat gct       191
   51 Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala
   52            50                  55                  60
   54 gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc       239
   55 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
   56       65                  70                  75
   58 act gcc tat ttg cag atc aag aag ctc aaa aat gag gac acg gct aca       287
   59 Thr Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr
   60 80                  85                  90                  95
   63 tat ttc tgt gga agg caa ttt att acc tac ggc ggg ttt gct aac tgg       335
   64 Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp
```

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65                100                105                110
67 ggc caa ggg act ctg gtc act gtc tct gca tcg agc tcc tcc gga tct   383
68 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser
69                115                120                125
71 tca tct agc ggt tcc agc tcg agc gat atc gtc atg acc cag tct cct   431
72 Ser Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro
73           130                135                140
75 aaa ttc atg tcc acg tca gtg gga gac agg gtc agc atc tcc tgc aag   479
76 Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys
77      145                150                155
79 gcc agt cag gat gtg agt act gct gta gcc tgg tat caa caa aaa cca   527
80 Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
81 160                165                170                175
83 ggg caa tct cct aaa cta ctg att tac tgg aca tcc acc cgg cac act   575
84 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr
85                180                185                190
87 gga gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat tat act   623
88 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr
89                195                200                205
91 ctc acc atc agc agt gtg cag gct gaa gac ctg gca ctt cat tac tgt   671
92 Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys
93           210                215                220
95 cag caa cat tat aga gtg ccg tac acg ttc gga ggg ggg acc aag ctg   719
96 Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
97      225                230                235
99 gag ata aaa cgg gct gat ggg gga ggt gga tgt taacggggga ggtggatgtt   772
100 Glu Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys
101 240                245                250
103 gggtctcgtt acgttgcgga tctcgaggct atctttacta actcttaccg taaagttctg    832
105 gctcaactgt ctgcacgcaa gcttttgcag gatatcatga gcgcttaaga tccgtcgacc    892
107 tgcaggcatg caagctt                                                   909
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112 <212> TYPE: PRT
113 <213> ORGANISM: Artificial Sequence
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116 <223> OTHER INFORMATION: 741F8 sFv'
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121 1                5                10                15
125 Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
126                20                25                30
129 Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys
130           35                40                45
133 Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu
134      50                55                60
137 Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr
138 65                70                75                80
141 Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr Tyr
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Output Set: N:\CRF3\06182002\I558741.raw

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145 Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly
146              100             105             110
149 Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser
150          115             120             125
153 Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys
154      130             135             140
157 Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala
158 145             150             155             160
161 Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
162              165             170             175
165 Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
166              180             185             190
169 Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
170          195             200             205
173 Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln
174      210             215             220
177 Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
178 225             230             235             240
181 Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys
182          245             250
185 <210> SEQ ID NO: 3
186 <211> LENGTH: 779
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: 26-10 sFv'
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194 <222> LOCATION: (3)..(758)
195 <223> OTHER INFORMATION:
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200    Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro
201    1               5                   10                  15
203 ggc gcc tct gtg cgc atg tcc tgc aaa tcc tct ggg tac att ttc acc        95
204 Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr
205                  20              25                  30
207 gac ttc tac atg aat tgg gtt cgc cag tct cat ggt aag tct cta gac       143
208 Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp
209              35              40                  45
211 tac atc ggg tac att tcc cca tac tct ggg gtt acc ggc tac aac cag       191
212 Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln
213          50              55                  60
215 aag ttt aaa ggt aag gcg acc ctt act gtc gac aaa tct tcc tca act       239
216 Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
217      65              70                  75
219 gct tac atg gag ctg cgt tct ttg acc tct gag gac tcc gcg gta tac       287
220 Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
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RAW SEQUENCE LISTING   DATE: 06/18/2002
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Input Set : N:\Crf3\Datahold\EFS\09558741\CIBT-P01-130SequenceListing.txt
Output Set: N:\CRF3\06182002\I558741.raw

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221 80                    85                90                95
223 tat tgc gcg ggc tcc tct ggt aac aaa tgg gcc atg gat tat tgg ggt        335
224 Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly
225                       100               105               110
227 cat ggt gct agc gtt act gtg agc tcc tcc gga tct tca tct agc ggt        383
228 His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly
229                       115               120               125
231 tcc agc tcg agt gga tcc gac gtc gta atg acc cag act ccg ctg tct        431
232 Ser Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser
233                       130               135               140
235 ctg ccg gtt tct ctg ggt gac cag gct tct att tct tgc cgc tct tcc        479
236 Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
237         145               150               155
239 cag tct ctg gtc cat tct aat ggt aac act tac ctg aac tgg tac ctg        527
240 Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu
241 160                   165               170               175
243 caa aag gct ggt cag tct ccg aag ctt ctg atc tac aaa gtc tct aac        575
244 Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn
245                       180               185               190
247 cgc ttc tct ggt gtc ccg gat cgt ttc tct ggt tct ggt tct ggt act        623
248 Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
249                       195               200               205
251 gac ttc acc ctg aag atc tct cgt gtc cag gcc gaa gac ctg ggt atc        671
252 Asp Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile
253         210               215               220
255 tac ttc tgc tct cag act act cat gta ccg ccg act ttt ggt ggt ggc        719
256 Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly
257         225               230               235
259 acc aag ctc gag att aaa cgt tcc ggg gga ggt gga tgt taactgcagc        768
260 Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
261 240                   245               250
263 ccggggggatc c                                                          779
266 <210> SEQ ID NO: 4
267 <211> LENGTH: 252
268 <212> TYPE: PRT
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: 26-10 sFv'
274 <400> SEQUENCE: 4
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277 1                     5                 10                15
280 Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp
281                       20                25                30
284 Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr
285             35                40                45
288 Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys
289         50                55                60
292 Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
293 65                    70                75                80
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RAW SEQUENCE LISTING   DATE: 06/18/2002
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Input Set : N:\Crf3\Datahold\EFS\09558741\CIBT-P01-130SequenceListing.txt
Output Set: N:\CRF3\06182002\I558741.raw

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296 Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
297             85              90              95
300 Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His
301             100             105             110
304 Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser
305             115             120             125
308 Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
309     130             135             140
312 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
313 145             150             155             160
316 Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln
317             165             170             175
320 Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
321             180             185             190
324 Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
325             195             200             205
328 Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile Tyr
329     210             215             220
332 Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr
333 225             230             235             240
336 Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
337             245             250
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341 <211> LENGTH: 739
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <223> OTHER INFORMATION: 520C9 sFv
348 <220> FEATURE:
349 <221> NAME/KEY: CDS
350 <222> LOCATION: (1)..(729)
351 <223> OTHER INFORMATION:
354 <400> SEQUENCE: 5
355 gag atc caa ttg gtg cag tct gga cct gag ctg aag aag cct gga gag      48
356 Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
357 1               5               10              15
359 aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc gca aac tat     96
360 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
361             20              25              30
363 gga atg aac tgg atg aag cag gct cca gga aag ggt tta aag tgg atg    144
364 Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
365             35              40              45
367 ggc tgg ata aac acc tac act gga cag tca aca tat gct gat gac ttc    192
368 Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe
369     50              55              60
373 aag gaa cgg ttt gcc ttc tct ttg gaa acc tct gcc acc act gcc cat    240
374 Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His
375 65              70              75              80
377 ttg cag atc aac aac ctc aga aat gag gac tcg gcc aca tat ttc tgt    288
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VERIFICATION SUMMARY   DATE: 06/18/2002
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Input Set : **N:\Crf3\Datahold\EFS\09558741\CIBT-P01-130SequenceListing.txt**
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